Chapter 4: 4.3, 4.7, 4.13, 4.18, 4.22

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March 29, 2018

4.3

```
library(readxl)
cloth <- read_excel("cloth.xlsx")</pre>
clothLong=reshape(cloth,
                     varying = c("Bolt1", "Bolt2", "Bolt3",
                                "Bolt4", "Bolt5"),
                     v.names = "Yield", timevar = "Bolt",
                     direction = "long")
cloth.aov=aov(Yield ~ factor(Bolt) + factor(Chemical), data = clothLong)
summary(cloth.aov)
                    Df Sum Sq Mean Sq F value
                                                Pr(>F)
                     4 157.00 39.25 21.606 2.06e-05 ***
## factor(Bolt)
## factor(Chemical) 3 12.95
                                 4.32
                                        2.376
                                                 0.121
## Residuals
                   12 21.80
                                 1.82
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
MSe=summary(cloth.aov)[[1]][3,3]
H_0: T_1 = \dots = T = p = 0
```

From our ANOVA we see that our chemical has an f-value of 2.376 with a p-value = 0.121. Our p-value is too big so we must fail to reject our null hypothesis and conclude that there is no differences between the treatment/chemical types.

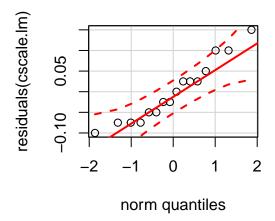
4.7

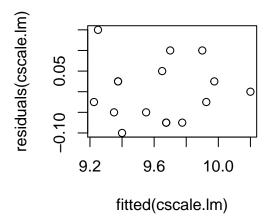
 $H_1: T_i \neq 0$ at least one.

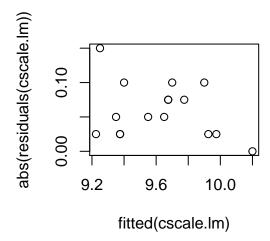
(a)

```
cscale.aov=aov(Yield ~ factor(Coupon) + factor(Tip), data = cscaleLong)
summary(cscale.aov)
                  Df Sum Sq Mean Sq F value
##
                                               Pr(>F)
## factor(Coupon) 3 0.825 0.27500 30.94 4.52e-05 ***
## factor(Tip)
                   3 0.385 0.12833
                                       14.44 0.000871 ***
## Residuals
                   9 0.080 0.00889
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
MSe=summary(cscale.aov)[[1]][3,3]
H_0: T_1 = ... = T = p = 0
_{
m VS}
H_1: T_i \neq 0 at least one.
Based on our ANOVA we see that we have a f-value of 14.44 and a p-value of 0.000871. Our p-value is
very small compare to the significance value so we must reject our null hypothesis and conclude that the
treatment/tips are significantly different.
ybar.trt=as.vector(with(cscaleLong, tapply(Yield,Tip,function(x) mean(x)))) #bar(Y_i.) vector
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[1]-ybar.trt[2])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.7163449
#1-3
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[1]-ybar.trt[3])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.09354966
#1-4
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[1]-ybar.trt[4])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.001488949
#2-3
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[2]-ybar.trt[3])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.05100326
#2-4
a=4;b=4;N=a*b;alpha=0.05
```

```
t0=(ybar.trt[2]-ybar.trt[4])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.002578639
#3-4
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[3]-ybar.trt[4])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.0001290132
While using Fisher LSD we output a pvalue for the compariosns of \mu_1 = \mu_2, \mu_1 = \mu_3, \mu_1 = \mu_4, \mu_2 = \mu_3,
\mu_2 = \mu_4, and \mu_3 = \mu_4 and the results are presented above respectively. We see that the comparisons of
\mu_1 = \mu_4, \mu_2 = \mu_4, and \mu_3 = \mu_4 are different in tips of mean hardness.
 (c)
##
## Call:
## lm(formula = Yield ~ factor(Coupon) + factor(Tip), data = cscaleLong)
## Residuals:
##
        Min
                  1Q
                       Median
                                     3Q
## -0.10000 -0.05625 -0.01250 0.03125 0.15000
##
## Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                               0.06236 149.934 < 2e-16 ***
                    9.35000
## factor(Coupon)2 0.02500
                                0.06667
## factor(Coupon)3 0.32500
                                        4.875 0.000877 ***
## factor(Coupon)4 0.55000
                                0.06667
                                        8.250 1.73e-05 ***
## factor(Tip)2
                    0.02500
                                0.06667
                                        0.375 0.716345
## factor(Tip)3
                   -0.12500
                                0.06667 -1.875 0.093550 .
## factor(Tip)4
                    0.30000
                                0.06667
                                        4.500 0.001489 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.09428 on 9 degrees of freedom
## Multiple R-squared: 0.938, Adjusted R-squared: 0.8966
## F-statistic: 22.69 on 6 and 9 DF, p-value: 5.933e-05
```







After observing the qqplot and residual plot we see that normality is fine and there is no pattern but a structureless image on our plot. We can conclude our model is good.

4.13

```
"Time4", "Time5", "Time6"),
v.names = "Yield", timevar = "Time",
direction = "long")
```

(a)

```
rbdvolt.aov=aov(Yield ~ factor(Ratio.Control) + factor(Time), data = rbdvoltLong)
summary(rbdvolt.aov)
```

 $H_1: T_i \neq 0$ at least one.

We look at our ANOVA and pay close attention to our results in terms of ratio control. We have a f-value of 0.190 and a p-value too big of 0.901. We fail to reject our null hypothesis and conclude that ratio control does not affect voltage.

(b)

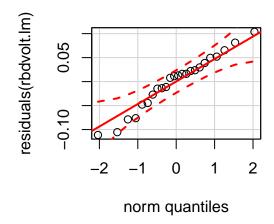
```
rbdsd.aov=aov(Yield ~ factor(Ratio.Control) + factor(Time), data = rbdsdLong)
summary(rbdsd.aov)
```

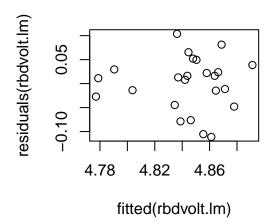
```
## Df Sum Sq Mean Sq F value Pr(>F) ## factor(Ratio.Control) 3 0.026013 0.008671 50.756 4.34e-08 *** ## factor(Time) 5 0.002721 0.000544 3.185 0.0371 * ## Residuals 15 0.002563 0.000171 ## --- ## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 H_0: T_1 = \ldots = T = p = 0
```

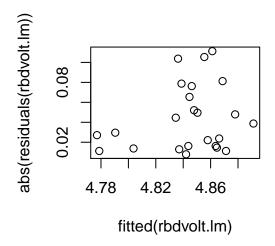
 $H_1: T_i \neq 0$ at least one.

From the ANOVA, observing the standard deviation of Voltage we see that we have f-value of 50.756 and a very small p-value of 4.34e-08 for ratio control. We reject our null hypothesis and conclude that ratio control does affect standard deviation or "pot noise".

(c)







By performing a qqplot and residual plots we see that normality is up to check and our residual plot is a structureless pattern which means that our model is good.

(d)

From the first algorithm we were unsuccessful to reduce the voltage, on the other hand on algorithm two we manage to reduce the SD or Pot Noise successfully. It is best to choose algorithm 2.

4.18

```
## Residuals
                   11 21.76
                                1.98
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## 1 observation deleted due to missingness
x=predict(aov(Yield ~ factor(Chemical) + factor(Bolt), clothMissing), newdata = clothLong["2.3", ]); x
##
      1
## 75.25
#72.25
clothImpute=clothMissing
clothImpute["2.3", "Yield"]=75.25
a=aov(Yield ~ factor(Chemical) + factor(Bolt), clothImpute)
summary(a)
                   Df Sum Sq Mean Sq F value
##
                                               Pr(>F)
## factor(Chemical) 3 12.78
                                4.26
                                        2.35
                                                0.124
## factor(Bolt)
                    4 158.89
                               39.72
                                       21.90 1.92e-05 ***
## Residuals
                   12 21.76
                                1.81
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
a$df.residual=a$df.residual - 1 #important: correction of df!
summary(a)
##
                   Df Sum Sq Mean Sq F value
                                               Pr(>F)
## factor(Chemical) 3 12.78
                                4.26
                                       2.154
                                                0.151
## factor(Bolt)
                    4 158.89
                               39.72 20.078 5.14e-05 ***
## Residuals
                   11 21.76
                                1.98
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Using R we are able to set the missing value as x and solve it, which results to 75.25. In which this value gives us the minimum error. As we can see from our new anova we see that all p-values and f-values are to check and can confirm this model is a good model.

4.22

```
library(readxl)
chemical <- read_excel("chemical.xlsx")</pre>
matrix(chemical$Ingrediants, 5,5)
##
        [,1] [,2] [,3] [,4] [,5]
## [1,] "a"
             "b"
                  "d"
                        "c"
                             "e"
## [2,] "c"
             "e"
                   "a"
                             "b"
                        "d"
## [3,] "b"
             "a"
                   "c"
                        "e"
                             "d"
## [4,] "d"
             "c"
                  "e"
                        "b"
             "d"
                  "b"
                        "a"
## [5,] "e"
matrix(chemical$Reaction.Time, 5,5)
        [,1] [,2] [,3] [,4] [,5]
## [1,]
          8
              7
                     1
                           7
```

```
## [2,]
                2
                     7
                                8
          11
                          3
## [3,]
                9
           4
                    10
                          1
                               5
## [4,]
           6
                8
                     6
                           6
                               10
## [5,]
           4
                2
                     3
                          8
                                8
summary(aov(Reaction.Time ~ factor(Batch) + factor(Day) + Ingrediants, chemical))
##
                 Df Sum Sq Mean Sq F value
                                              Pr(>F)
## factor(Batch)
                    12.24
                               3.06
                                      0.979 0.455014
## factor(Day)
                               3.86
                                      1.235 0.347618
                    15.44
## Ingrediants
                  4 141.44
                              35.36
                                     11.309 0.000488 ***
## Residuals
                 12 37.52
                               3.13
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
H_0: T_1 = \dots = T = p = 0
```

 $H_1: T_i \neq 0$ at least one.

Based on our ANOVA we see that our treatment has a f-value of 11.309 with a p-value of 0.000488. Our p-value is very small and we reject our null hypothesis. We can state that chemical process and time of day have an affect on our ingredients (A,B,C,D,E).